SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: SAMSON, MICHEL PARMENTIER, MARC VASSART, GILBERT LIBERT, FREDERICK
 - (ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
 - (iii) NUMBER OF SEQUENCES: 17
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Knobbe, Martens, Olson & Bear
 - (B) STREET: 620 Newport Center Drive 16th Floor
 - (C) CITY: Newport Beach
 - (D) STATE: CA

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- (E) COUNTRY: U.S.A.
- (F) ZIP: 92660
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/833,752
 - (B) FILING DATE: 9-APR-1997
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Altman, Daniel E
 - (B) REGISTRATION NUMBER: 34,115
 - (C) REFERENCE/DOCKET NUMBER:
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 240..791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCCCTTCACT ACTATGTAGGCA AT	AAAACTTC ATTG TAAAAAACC TATT	CTTGGC CAAAAAGAG GATGTA TAAAACAGT	CA GGGAAGCTAG CAGCAAACCT 60 GA GTTAATTCAA TGTAGACATC 120 TT TGCATTCATG GAGGGCAACT 180
ATG GAT TAT C	AA GTG TCA AG	T CCA ATC TAT GA	TT ATGCACAGGG TGGAACAAG 239 AC ATC AAT TAT TAT ACA 287 sp Ile Asn Tyr Tyr Thr 15
			AA ATC GCA GCC CGC CTC 335 In Ile Ala Ala Arg Leu 30
			TT GGT TTT GTG GGC AAC 383 ne Gly Phe Val Gly Asn 45
		u Ile Asn Cys Ly	AA AGG CTG AAG AGC ATG 431 vs Arg Leu Lys Ser Met 60
ACT GAC ATC T		n Leu Ala Ile Se	CT GAC CTG TTT TTC CTT 479 er Asp Leu Phe Phe Leu 75 80
8			CC GCC CAG TGG GAC TTT 527 La Ala Gln Trp Asp Phe 95
Gly Asn Thr M			TC TAT TTT ATA GGC TTC 575 eu Tyr Phe Ile Gly Phe 110
			CA ATC GAT AGG TAC CTG 623 or Ile Asp Arg Tyr Leu 125
		e Ala Leu Lys Al	CC AGG ACG GTC ACC TTT 671 a Arg Thr Val Thr Phe 140
			TG GCT GTG TTT GCG TCT 719 al Ala Val Phe Ala Ser 55 160
			AA GAA GGT CTT CAT TAC 767 vs Glu Gly Leu His Tyr 175
Thr Cys Ser S	CT CAT TTT CC er His Phe Pr 80		792

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1477 base pairs
- (B) TYPE: nucleic acid(C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 240..1295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAA:	rtcc	CCC .	AACA	GAGC	CA A	GCTC'	TCCA'	r cti	AGTG	GACA	GGG	AAGC'	TAG	CAGC	AAACCT	60
TCC	CTTC	ACT A	ACAA	AACT'	TC A'	TTGC'	TTGG(C CA	AAAA	GAGA	GTT	TTAA	CAA	TGTA	GACATC	120
TAT	FTAG(GCA 2	ATTA	AAAA	CC T	ATTG	ATGT	A TA	AAAC	AGTT	TGC	ATTC	ATG	GAGG	GCAACT	180
AAA.	raca:	TTC '	TAGG	ACTT'	TA T	AAAA	GATC	A CT	TTTT.	TTTA	ATG	CACA	GGG '	TGGA	ACAAG	239
														TAT		287
														Tyr		
a.		_		5					10	-			-	15		
TCG	GAG	CCC	TGC	CAA	AAA	ATC	AAT	GTG	AAG	CAA	ATC	GCA	GCC	CGC	CTC	335
Ser	Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	
			20		_			25	-				30			
CTG	CCT	CCG	CTC	TAC	TCA	CTG	GTG	TTC	ATC	TTT	GGT	TTT	GTG	GGC	AAC	383
Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	
		35					40				_	45		_		
ATG	CTG	GTC	ATC	CTC	ATC	CTG	ATA	AAC	TGC	AAA	AGG	CTG	AAG	AGC	ATG	431
Met	Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Arg	Leu	Lys	Ser	Met	
- W	50					55					60		_			
ACT	GAC	ATC	TAC	CTG	CTC	AAC	CTG	GCC	ATC	TCT	GAC	CTG	TTT	TTC	CTT	479
Thr	Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Phe	Phe	Leu	
65					70					75	_				80	
CTT	ACT	GTC	CCC	TTC	TGG	GCT	CAC	TAT	GCT	GCC	GCC	CAG	TGG	GAC	TTT	527
Leu	Thr	Val	Pro	Phe	Trp	Ala	His	Tyr	Ala	Ala	Ala	Gln	Trp	Asp	Phe	
				85					90					95		
GGA.	AAT	ACA	ATG	TGT	CAA	CTC	TTG	ACA	GGG	CTC	TAT	TTT	ATA	GGC	TTC	575
Gly	Asn	Thr	Met	Cys	Gln	Leu	Leu	Thr	Gly	Leu	Tyr	Phe	Ile	Gly	Phe	
			100					105					110	-		
TTC	TCT	GGA	ATC	TTC	TTC	ATC	ATC	CTC	CTG	ACA	ATC	GAT	AGG	TAC	CTG	623
Phe	Ser		Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	
		115					120					125				
GCT	GTC	GTC	CAT	GCT	GTG	TTT	GCT	TTA	AAA	GCC	AGG	ACG	GTC	ACC	TTT	671
Ala	Val	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	,
	130					135					140					
GGG	GTG	GTG	ACA	AGT	GTG	ATC	ACT	TGG	GTG	GTG	GCT	GTG	TTT	GCG	TCT	719
Gly	Val	Val	Thr	Ser		Ile	Thr	Trp	Val	Val	Ala	Val	Phe	Ala	Ser	
145					150					155					160	
CTC	CCA	GGA	ATC	ATC	TTT	ACC	AGA	TCT	CAA	AAA	GAA	GGT	CTT	CAT	TAC	767
Leu	Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser		Lys	Glu	Gly	Leu	His	Tyr	
				165					170					175		

											CAA					815
Thr	Cys	Ser		His	Phe	Pro	Tyr		Gln	Tyr	Gln	Phe		Lys	Asn	
			180					185					190			
											GTC					863
Phe	Gln		Leu	Lys	Ile	Val		Leu	Gly	Leu	Val		Pro	Leu	Leu	
		195					200					205				
											ACT					911
Val		Val	Ile	Cys	Tyr		Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys	
	210					215					220					
											CTT					959
	Asn	Glu	Lys	Lys	_	His	Arg	Ala	Val	Arg	Leu	Ile	Phe	Thr		
225					230					235					240	
											AAC				CTC	1007
Met	Ile	Val	Tyr		Leu	Phe	\mathtt{Trp}	Ala	Pro	Tyr	Asn	Ile	Val	Leu	Leu	
				245					250					255		
											AAT					1055
Leu	Asn	Thr		Gln	Glu	Phe	Phe	-	Leu	Asn	Asn	Cys		Ser	Ser	
23 60%			260					265					270			
											ACT					1103
Asn	Arg		Asp	GIn	Ala	Met		Val	Thr	Glu	Thr		GLY	Met	Thr	
LIF THE COLUMN		275			~~~		280					285				
											GTC					1151
- 150	-	Cys	ile	Asn	Pro		TTE	Tyr	Ala	Phe	Val	GIY	Glu	гàг	Pne	
	290	m 7 C	ama.		ama.	295	mma	C 7 7	770	G 7 G	300	~~~		999		4400
											ATT				TTC	1199
305	ASII	Tyr	ьeu	ьeu		Pne	Pne	GIN	гуѕ		Ile	AIa	гля	Arg		
**	7 7 7	maa	mom.	mam	310	mma	an a	(17.7	ara	315	CCC	aza	aa x	003	320	1045
2											Pro					1247
Cya	цур	Cys	Cys	325	TIE	Pile	GIII	GIII	330	АŢĢ	PIO	GIU	Arg	335	ser	
الأدات	CTT	ጥ አ ር	אככ		TCC	አ ርጥ	ccc	GNG		C 7 7	ATA	th Cate	CTC		TTC	1295
											Ile					1295
	val	TYL	340	AT 9	Ser	TIIT	Gry	345	GIII	Giu	TIE	SET	350	GTĀ	ьеи	
TGÁ	'ACGC	ימר יו		TGGG	с то	CTCZ	יככב		ממממי	בידידיכי	TGCZ	ער א ייינ		רידי א כייוי	TTTCA	1355
															CTGTTA	1415
															CCGAAT	1475
TC		4						. JCF	-1010		- 11 31-3C	LINUT		*0*31	COATI	1477

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 240..884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCCCT	TCACT AGGCA	ACAA ATTA	AACT' AAAA	TC A CC T	TTGC' ATTG	TTGG(ATGT <i>I</i>	C CA. A TA.	AAAA AAAC	GAGA AGTT	GTT. TGC	AATTC	CAA ATG	TGTA(GAGG(AAACCT GACATC GCAACT	60 120 180
ATG G	מיד ידמ	ממיז יד	CTC	יירם.	ልርጥ	CCA	איזיירי	ተተተተ	GAC	איזיכי	ית א תא	יייאריי	ייי עידי	ACAAG	239
Met As															287
	sb i	r Giii	vai	Ser	Ser	PIO	тте	_	Asp	тте	ASII	TAL	_	Tnr	
1		~ =~	5					10					15		
TCG G	AG CC	C TGC	CAA	AAA	ATC	AAT	GTG	AAG	CAA	ATC	GCA	GCC	CGC	CTC	335
Ser G	lu Pr	o Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	
		20					25					30			
CTG CO	CT CC	G CTC	TAC	TCA	CTG	GTG	TTC	ATC	TTT	GGT	TTT	GTG	GGC	AAC	383
Leu Pi	ro Pro	o Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Glv	Phe	Val	Glv	Asn	
	3	5	-			40				1	45		1		
ATG_C			CTC	ATC	CTG		ΔΔC	TGC	מממ	» CC		λλG	አርር	እ ጥ ር	121
Met[]Le	en Va	l Tle	Len	Tle	T.011	Tla	λan	Cvc	Tara	7~~	TOU	Luc	Cox	Mot	431
	En Va.		пси	110	55	TIG	WOII	Cys	пås	_ :	ьеu	nys	ser	Met	
		י יייארי	CTIC	CTC		CITIC	aaa	3 111 (1	mam	60	OTT C	mmm	mma	amm	
ACT GA	AC AI	- TAC	CIG	CIC	AAC	CIG	GCC	ATC	TCT	GAC	CIG	TTT	TTC	CTT	479
ThraAs	sp II	e Tyr	ьeu	Leu	Asn	ьeu	Ala	TTE		Asp	Leu	Phe	Phe		
65.				70					75					80	
CTT AC	CT GT	CCC	TTC	TGG	GCT	CAC	TAT	GCT	GCC	GCC	CAG	TGG	GAC	$ ext{TTT}$	527
Leu Th	nr Val	l Pro	Phe	Trp	Ala	His	Tyr	Ala	Ala	Ala	Gln	Trp	Asp	Phe	
9			85					90					95		
GGA AZ	AT AC	A ATG	TGT	CAA	CTC	TTG	ACA	GGG	CTC	TAT	TTT	ATA	GGC	TTC	575
Gly As	sn Th	r Met	Cys	Gln	Leu	Leu	Thr	Glv	Leu	Tvr	Phe	Ile	Glv	Phe	
Ti fat		100	-				105	1	,	- 1 -		110			
TTCTTC	CT GG		TTC	TTC	ATC	ATC		CTG	מרמ	ΔΤΟ	СДТ	AGG	ጥልሮ	CTC	623
Phe Se	er Gla	, Tle	Phe	Phe	Tla	Tla	T.OII	LOU	Thr	TIO) an	7×~	Tree	Ton	023
	11!	, 110	1110	1110	110	120	пец	пец	TIIL	TTG		ALG	TAT	пеп	
CC Think CT			CCT	CTC	מוחות		מיחים	777	aaa	3.00	125	ama	3.00	mmm	c == a
GCT GI	77 772	CAL	77-	77-7	111	37-	IIA	AAA	37	AGG	ACG	GIC	ACC	TTT	671
Ala Va	ar va.	L HIS	ALA	var	Pne	Ala	ьeu	ьys	Ala		Thr	Val	Thr	Phe	
13			. ~-	~~~	135					140					
GGG GI	rg Gr	3 ACA	AGT	GTG	ATC	ACT	TGG	GTG	GTG	GCT	GTG	TTT	GCG	TCT	719
Gly Va	al Val	l Thr	Ser	Val	Ile	Thr	Trp	Val	Val	Ala	Val	Phe	Ala	Ser	
145				150					155					160	
CTC CC	CA GGA	ATC	ATC	TTT	ACC	AGA	TCT	CAA	AAA	GAA	GGT	CTT	CAT	TAC	767
Leu Pr	co Gly	/ Ile	Ile	Phe	Thr	Arg	Ser	Gln	Lys	Glu	Gly	Leu	His	Tyr	
-			165			_		170	•		•		175	•	
ACC TG	C AG	TCT	CAT	TTT	CCA	TAC	ATT		GAT	AGT	CAT	CTT		GCT	815
Thr Cy	s Sei	Ser	His	Phe	Pro	Tvr	Tle	Lvs	Asn	Ser	Hig	T.e.11	Glv	Δla	013
2		180				-1-	185	Lyo	1100		1110	190	Ory	nia	
GGT CC	יד פרנ		CCT	ጥርጥ	$C \lambda T$	CCT	TOO	CTC	COLV	CTC	aaa	7 7 T	CCT	73.73.73	863
Gly Dr	$\sim \lambda l$	712	חוסט	Cva	Uia	GG1	CMI	T	CIA	CIC	07	AAI	CCI	AAA	863
Gly Pr	.U A16	HIA	нта	Cys	HIS		HIS	Leu	ьeu	ьeu		Asn	Pro	гÀз	
7 7 C TC			ama	maa		200					205			_	
AAC TO	-1 GC1	. 106	GIG	100	AAA	TGAG	AAGA	AG A	AGGCA	CAG	G CI	ľĠľĠ	AGGCI	•	914
Asn Se		Ser	Val	Ser	_										
21					215										
TATCTT	CACC	ATCAT	'GAT'I	G TI	TATT	TTCT	' CTI	CTGG	GCT	CCCI	ACAP	ACA 1	TGTC	CTTCT	974

CCTGAACACC TTCCAGGAAT	TCTTTGGCCT	GAATAATTGC	AGTAGCTCTA	ACAGGTTGGA	1034
CCAAGCTATG CAGGTGACAG	AGACTCTTGG	GATGACGCAC	TGCTGCATCA	ACCCCATCAT	1094
CTATGCCTTT GTCGGGGAGA	AGTTCAGAAA	CTACCTCTTA	GTCTTCTTCC	AAAAGCACAT	1154
TGCCAAACGC TTCTGCAAAT	GCTGTTCTAT	TTTCCAGCAA	GAGGCTCCCG	AGCGAGCAAG	1214
CTCAGTTTAC ACCCGATCCA					1274
CAAGTGGGCT GGTGACCCAG	TCAGAGTTGT	GCACATGGCT	TAGTTTTCAT	ACACAGCCTG	1334
GGCTGGGGGT GGTTGGGAGG	TCTTTTTTAA	AAGGAAGTTA	CTGTTATAGA	GGGTCTAAGA	1394
TTCATCCATT TATTTGGCAT	CTGTTTAAAG	TAGATTAGAT	CCGAATTC		1442

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 184 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

7 7															
Metu <i>l</i>	Asp	Tyr	Gln	Val 5	Ser	Ser	Pro	Ile	Tyr 10	Asp	Ile	Asn	Tyr	Tyr 15	Thr
Ser C	Glu	Pro	Cys 20	Gln	Lys	Ile	Asn	Val 25	Lys	Gln	Ile	Ala	Ala 30	Arg	Leu
Leu	Pro	Pro 35	Leu	Tyr	Ser	Leu	Val 40	Phe	Ile	Phe	Gly	Phe 45	Val	Gly	Asn
Met-I	Leu 50	Val	Ile	Leu	Ile	Leu 55	Ile	Asn	Cys	Lys	Arg 60	Leu	Lys	Ser	Met
Thr. 7	4sp	Ile	Tyr	Leu	Leu 70	Asn	Leu	Ala	Ile	Ser 75	Asp	Leu	Phe	Phe	Leu 80
Leu	Thr	Val	Pro	Phe 85	Trp	Ala	His	Tyr	Ala 90	Ala	Ala	Gln	Trp	Asp 95	Phe
Gly I	Asn	Thr	Met 100	Cys	Gln	Leu	Leu	Thr 105	Gly	Leu	Tyr	Phe	Ile 110	Gly	Phe
Phe S	Ser	Gly 115	Ile	Phe	Phe	Ile	Ile 120	Leu	Leu	Thr	Ile	Asp 125	Arg	Tyr	Leu
Ala V	/al L30	Val	His	Ala	Val	Phe 135	Ala	Leu	Lys	Ala	Arg 140	Thr	Val	Thr	Phe
Gly V 145	/al	Val	Thr	Ser	Val 150	Ile	Thr	Trp	Val	Val 155	Ala	Val	Phe	Ala	Ser 160
Leu E	Pro	Gly	Ile	Ile 165	Phe	Thr	Arg	Ser	Gln 170		Glu	Gly	Leu	His 175	
Thr C	Cys	Ser	Ser 180	His	Phe	Pro	Tyr		· -						

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

1			Gln	5					10					15	
Ser	Glu	Pro	Cys 20	Gln	Lys	Ile	Asn	Val 25		Gln	Ile	Ala	Ala 30	Arg	Leu
Leu	Pro	Pro 35	Leu	Tyr	Ser	Leu	Val 40		Ile	Phe	Gly	Phe 45	Val	Gly	Asn
	50		Ile			55					60				
65			Tyr		70					75					80
			Pro	85					90					95	Phe
ŁD.			Met 100					105					110	Gly	
i.i.i		TTD	Ile				120					125			
٩	130		His			135					140				
145			Thr		150					155					160
2=1			Ile	165					170					175	Tyr
86.3			Ser 180					185					190		
777		195	Leu				200					205			
-	ZTO		Ile			215					220				
225			Lys		230					235					240
			Tyr	245					250					255	
			Phe 260					265					270		
		275	Asp				280					285			
	230		Ile			295					300				
505			Leu		3 I U					315					320
			Cys	325					330					Ala 335	Ser
ser	val	Tyr	Thr 340	Arg	Ser	Thr	Gly	Glu 345	Gln	Glu	Ile	Ser	Val 350	Gly	Leu

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr 10 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arq Leu 25 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met 55 Tha Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu Lew Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe 85 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 100 105 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 115 120 125 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 135 140 Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 145 150 155 Lew Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 170 Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala 185 Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys 200 205 Asn Ser Ala Ser Val Ser Lys 210 215

- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
                                     10
Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
                             40
Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
                     70
Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Ile Thr Leu Pro
                                     90
Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
                                 105
Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
        115
                             120
Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
                         135
                                             140
Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
                    150
                                         155
Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
                165
                                     170
Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
            180
                                 185
Typ Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
        195
                             200
Lew Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
                        215
Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
                    230
                                         235
Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
                245
                                     250
    Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
                                 265
            260
                                                     270
Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Ile Gln
                             280
                                                 285
Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
                        295
                                             300
Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Ile Ser Val Phe Phe
                    310
                                         315
Arg Lys His Ile Xaa Xaa Xaa Phe Cys Lys Gln Cys Pro Val Phe Tyr
                325
                                     330
Arg Glu Thr Val Asp Gly Val Thr Ser Thr Asn Thr Pro Ser Thr Gly
            340
                                 345
                                                     350
Glu Gln Glu Val Ser Ala Gly Leu
        355
                             360
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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met 1	Thr	Thr	Ser	Ile 5	Asp	Thr	Val	Glu	Thr 10	Phe	Gly	Thr	Thr	Ser 15	Tyr
Tyr	Asp	Asp	Val 20	Gly	Leu	Leu	Cys	Glu 25	Lys	Ala	Asp	Thr	Arg 30	Ala	Leu
Met	Ala	Gln 35	Phe	Val	Pro	Pro	Leu 40		Ser	Leu	Val	Phe 45	Thr	Val	Gly
Leu	Ile 50	Gly	Asn	Val	Val	Val 55	Val	Met	Ile	Leu	Ile 60	Lys	Tyr	Arg	Arg
Ile 65	Arg	Ile	Met	Thr	Asn 70	Ile	Tyr	Leu	Leu	Asn 75	Leu	Ala	Ile	Ser	Asp 80
Leu	Leu	Phe	Ile	Val 85	Thr	Leu	Pro	Phe	Trp 90	Thr	His	Tyr	Val	Arg 95	Gly
His	Asn	Trp	Val 100	Phe	Gly	His	Gly	Met 105	Cys	Asn	Leu	Ile	Ser 110	Gly	Phe
Tyr	His	Thr 115	Gly	Leu	Tyr	Ser	Glu 120	Ile	Phe	Phe	Ile	Ile 125	Leu	Leu	Thr
Ile	130	_				135					140			Arg	
Arg 145					150					155				Gly	160
m				165					170	,				Glu 175	
1 43			180			-		185		_			190	Thr	
Tyr	Ser	Trp 195	Arg	His	Phe	His	Thr 200	Ile	Arg	Met	Thr	Ile 205	Phe	Cys	Leu
Väl	Leu 210	Pro	Leu	Leu	Val	Met 215	Ala	Ile	Cys	Tyr	Thr 220	Gly	Ile	Ile	Lys
225			_	_	230				_	235	_			Arg	240
				245					250		_			Tyr 255	
			260				_	265					270	Asn	
		275					280					285		Glu	
	290				_	295					300			Phe	
Gly 305	Glu	Arg	Phe	Arg	Lys 310	Tyr	Ile	Arg	His	Phe 315	Phe	His	Arg	His	Leu 320
				325	-	-			330					Xaa 335	
Glu	Arg	Ile	Ser 340	Ser	Val	Ser	Pro	Ser 345	Thr	Ala	Glu	Pro	Glu 350	Ile	Ser
Ile	Val	Phe													

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe 25 GTy Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly 40 Lêu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg 55 Ligu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Ile Ser Gly Phe 105 Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr 120 The Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Ile Arg Ala 135 140 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Ile 150 155 Ala Ile Ile Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp 170 165 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu 185 Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu 205 195 200 Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Ile Gly Ile Ile Lys 210 220 215 Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu 235 230 Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Ile Pro Tyr Asn 245 250 255 Leu Thr Ile Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu 265 Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val 280 285 Ile Ala Tyr Thr His Cys Cys Val Asn Glu Val Ile Tyr Ala Phe Val 295

Gly Glu Arg Phe Arg Lys Tyr Ile Arg Gln Leu Glu His Arg Arg Val 305 310 315 320 Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Ile 325 330 335 Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Ile Ser 340 345 350 Ala Gly Phe 355

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu 25 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu Val Glu Val Phe Gly Leu Ile Gly Asn Ser Val Val Leu Val Leu The Lys Tyr Lys Arg Ile Arg Ser Met Thr Asp Val Tyr Leu Leu Asn 75 Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly 90 Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Ile Cys Lys Met 105 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val 120 Met Ile Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Glu 135 140 Xaa Xaa Xaa Ala Arg Thr Ile Ile Tyr Gly Val Ile Thr Ser Leu Ala 150 155 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Ile Phe Ser 165 170 Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser 185 Leu Asn Ser Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile 200 Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met 215 220 Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala 230 235 Val Lys Met Ile Phe Ala Val Val Leu Phe Leu Gly Phe Trp Thr

250 245 Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val 265 Ile Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala 275 280 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr 295 300 Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Ile Gln Leu Phe Lys 310 315 Xaa Xaa Xaa Gly Leu Phe Val Ile Cys Gln Tyr Cys Gly Leu Leu Gln 330 325 Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met 345 Asp His Asp Leu His Asp Ala Leu 355

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn PHe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu 25 Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys 40 35 Arg Asn Glu Lys Lys Arg 50

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTCCATACA GTCAGTATCA ATTCTGGAAG AATTTCCAGA CATTAAAGAT AGTCATCTTG 120 GGGCTGGTCC TGCCGCTGCT TGTCATGGTC ATCTGCTACT CGGGAATCCT AAAAACTCTG 147 CTTCGGTGTC GAAATGAGAA GAAGAGG

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(2) INFORMATION FOR SEQ ID NO:13:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala Gly Pro Ala Ala Ala 1 5 10 15	
Cys His Gly His Leu Leu Gly Asn Pro Lys Asn Ser Ala Ser Val 20 25 30	
Ser Lys	
(2) INFORMATION FOR SEQ ID NO:14:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14: TEGAGGATCC AAGATGGATT ATCAAGT (2) INFORMATION FOR SEQ ID NO:15:	۰.
TEGAGGATCC AAGATGGATT ATCAAGT	27
(2) INFORMATION FOR SEQ ID NO:15:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
CTGATCTAGA GCCATGTGCA CAACTCT	27
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTGGCTGTC GTCCATGCTG	20
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
CTGATCTAGA GCCATGTGCA CAACTCT	27